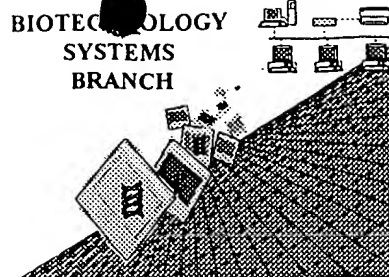# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____09/833,031_____

Source: _____O I P E_____

Date Processed by STIC: _____08/06/2001_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/833,031

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

```
    RAW SEQUENCE LISTING                              DATE: 08/06/2001
    PATENT APPLICATION:   US/09/833,031              TIME: 15:32:37

    Input Set : A:\Gilad2bl.app
    Output Set: N:\CRF3\08062001\I833031.raw

 3 <110> APPLICANT: GILAD, Shlomit
 4         EINAT, Paz
 5         GROSMAN, Avital
 7 <120> TITLE OF INVENTION: METHOD FOR ENRICHMENT OF NATURAL ANTISENSE MESSENGER
 8         RNA
10 <130> FILE REFERENCE: GILAD=2B
12 <140> CURRENT APPLICATION NUMBER: US/09/833,031
13 <141> CURRENT FILING DATE: 2001-04-11
15 <150> PRIOR APPLICATION NUMBER: 09/680,420
16 <151> PRIOR FILING DATE: 2000-10-06
18 <160> NUMBER OF SEQ ID NOS: 29
20 <170> SOFTWARE: PatentIn Ver. 2.1
 2 <210> SEQ ID NO: 1
 3 <211> LENGTH: 40
 4 <212> TYPE: DNA
15 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: n at position 40 represents g, a, c or t
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCOEOTIDE
32         PRIMERS
34 <400> SEQUENCE: 1
35 ttctagaatt cagcggccgc tttttttttt ttttttttvn                               40
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 22
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
45         PRIMERS
47 <400> SEQUENCE: 2
48 gatgggagtt gtgtgtttag tc                                                  22
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 22
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
58         PRIMERS
60 <400> SEQUENCE: 3
61 ggagagagaa gtgcagagtt cg                                                  22
64 <210> SEQ ID NO: 4
65 <211> LENGTH: 21
66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
```

Does Not Comply
Corrected Diskette Needed

OLIGONUCLEOTIDE (handwritten annotation)

C--> (line 12)
C--> (line 13)
W--> (line 35)

RAW SEQUENCE LISTING   DATE: 08/06/2001
PATENT APPLICATION: US/09/833,031   TIME: 15:32:37

Input Set : A:\Gilad2bl.app
Output Set: N:\CRF3\08062001\I833031.raw

```
71        PRIMERS
73 <400> SEQUENCE: 4
74 ttagtacaaa cttagggctc t                                      21
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 20
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
84        PRIMERS
86 <400> SEQUENCE: 5
87 tcatggcaac tccagagcag                                        20
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 20
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
97        PRIMERS
99 <400> SEQUENCE: 6
100 accacagtcc atgccatcac                                       20
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
110        PRIMERS
112 <400> SEQUENCE: 7
113 tccaccaccc tgttgctgta                                       20
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 22
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
123        PRIMERS
125 <400> SEQUENCE: 8
126 ggagttagtc cttgaccact ag                                    22
129 <210> SEQ ID NO: 9
130 <211> LENGTH: 22
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
136        PRIMERS
138 <400> SEQUENCE: 9
139 gcacttacac agttagtcat gg                                    22
142 <210> SEQ ID NO: 10
```

RAW SEQUENCE LISTING   DATE: 08/06/2001
PATENT APPLICATION: US/09/833,031   TIME: 15:32:37

Input Set : **A:\Gilad2bl.app**
Output Set: **N:\CRF3\08062001\I833031.raw**

```
143 <211> LENGTH: 188
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
149       SEQUENCE
151 <400> SEQUENCE: 10
152 gggcgggccg cttttttttt ttttttttttg gagttagtcc ttgaccacta gtttgatgcc 60
153 atctccattt tgggtgacct gtttcaccag caggcctgtt actctccatg actaactgtg 120
154 taagtgctta aaatggaata aattgctttt ctacataacc ccaaaaaaaa aaaaaaaaaa 180
155 gcggccgc                                                        188
158 <210> SEQ ID NO: 11
159 <211> LENGTH: 169
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
165       HUMAN
167 <400> SEQUENCE: 11
168 tttttttttt ttttttttgg agttagtcct tgaccactag tttgatgcca tctccatttt 60
169 gggtgacctg tttcaccagc aggcctgtta ctctccatga ctaactgtgt aagtgcttaa 120
170 aatggaataa attgcttttc tacataaccc caaaaaaaaa aaaaaaaa            169
173 <210> SEQ ID NO: 12
174 <211> LENGTH: 550
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
180       HUMAN
182 <220> FEATURE:
183 <223> OTHER INFORMATION: n at positions 114, 319, 340, 350, 369, 386, 455,
184       371, 506 and 538 are unknown.
186 <400> SEQUENCE: 12
187 ttttcattgt cataattttt tattatgtat caaattgtct tcaatataag ttacaacttg 60
188 attaaagttg atagacattt gtatctattt aaagacaaaa aaattctttt atgttcaata 120
189 tcttgtctag agtctagcaa atatagtacc tttcattgca ggatttctgc ttaatataac 180
190 aagcaaaand aaacaactga aaaaatataa accaaagcaa accaaacccc ccgctcaact 240
191 acaaatgtca atattgaatg aagcattaaa agacaaacat aaagtaactt cagcttttat 300
192 ctagcaatgc agaatgaatn ctaaaattag nggcaaaaaa ncaaacaaca aacaacaaac 360
193 aaaacaaanc aaacaancaa aaaatcccac caatcttcat gggtaaactt tcctgctcag 420
194 ggatgtaagc tgactctaga ccatcngcgg ttcctgcgga tagcacagcc angatcatc 480
195 gaagatcatg ccaaatntca tgaccacggc aatgccgatg cccctgcgcc gatgatgngg 540
196 aatttattgg                                                      550
199 <210> SEQ ID NO: 13
200 <211> LENGTH: 491
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
```

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 08/06/2001
PATENT APPLICATION: US/09/833,031   TIME: 15:32:37

Input Set : A:\Gilad2bl.app
Output Set: N:\CRF3\08062001\I833031.raw

```
206       HUMAN
208 <400> SEQUENCE: 13
209 tttttttttt ttttttttctt gctgcagcaa cgcgagtggg agcaccagga tctcgggctc 60
210 ggaacgagac tgcacggatt gttttaagaa aatggcagac aaaccagaca tgggggaaat 120
211 cgccagcttc gataaggcca agctgaagaa aacggagacg caggagaaga acaccctgcc 180
212 gaccaaagag accattgagc aggagaagcg gagtgaaatt tcctaagatc ctggaggatt 240
213 tcctacccccc atcctcttcg agaccccagt cgtgatgtgg aggaagagcc acctgcaaga 300
214 tggacacgag ccacaagctg cactgtgaac ctgggcactc cgtgccgatg ccaccggcct 360
215 gtgggtctct gaagggaccc ccccccaatc ggactgccaa attctccggt ttgccccggg 420
216 atattataga aaattatttg tatgaataat gaaaataaaa cacacctcgt ggcaaaaaaa 480
217 aaaaaaaaaa a                                                   491
220 <210> SEQ ID NO: 14
221 <211> LENGTH: 206
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
227       HUMAN
229 <400> SEQUENCE: 14
230 tttttttttt ttttttttgg gagtggtagg atgaaacaat ttggagaaga tagaagtttg 60
231 aagtggaaaa ctggaagaca gaagtacggg aaggcgaaga aaagaataga gaagataggg 120
232 aaattagaag ataaaaacat acttttagaa gaaaaaagat aaatttaaac ctgaaaagta 180
233 ggaagcagaa aaaaaaaaaa aaaaaa                                   206
236 <210> SEQ ID NO: 15
237 <211> LENGTH: 206
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
243       HUMAN
245 <220> FEATURE:
246 <223> OTHER INFORMATION: n at position 54 is unknown.          55 error
248 <400> SEQUENCE: 15
W--> 249 ttttctgtgg ggccatcact ttattaaggg gtcatctaga aggtgggccc cctgncaaac 60
250 cgcgggactg tgatcgggct ccagctactt caccaccccg ggccagcctg ctccaggggt 120
251 cccttcctgc tgagagcagg cgagaggcag tcaggctcat gaagcagcca ccgggtttgg 180
252 ctcactggaa ggaatcacac tggaaa                                   206
255 <210> SEQ ID NO: 16
256 <211> LENGTH: 178
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
262       HUMAN
264 <400> SEQUENCE: 16
265 tttttttttt ttttttttct gtgtccactg gagagcttga gctcacactc aaagatcaga 60
266 ggacctacag agagggctct ttggtttgag gaccatggct taccttttcct gcctttgacc 120
267 catcacaccc catttcctcc tctttccctc tccccgctgc caaaaaaaaa aaaaaaa 178
270 <210> SEQ ID NO: 17
```

RAW SEQUENCE LISTING   DATE: 08/06/2001
PATENT APPLICATION: US/09/833,031   TIME: 15:32:37

Input Set : A:\Gilad2bl.app
Output Set: N:\CRF3\08062001\I833031.raw

```
271 <211> LENGTH: 127
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
277       HUMAN
279 <220> FEATURE:
280 <223> OTHER INFORMATION: n at positions 98 and 112 are unknown.
282 <400> SEQUENCE: 17
283 gaattcgatg cgtattctgt ggcccgccat ctgcgcaggg tggtggtatt ctgccattta 60
284 cacacgtcgt tctaattaaa aagcgaatna tactccaaaa aaaaaaaaa angcggccgt 120
285 tgaattc                                                       127
288 <210> SEQ ID NO: 18
289 <211> LENGTH: 115
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
295       HUMAN
297 <400> SEQUENCE: 18
298 gaattcagcg gccgcttttt tttttttttt tcttcgaagt gtttacccca gtgtttgaaa 60
299 gggattccag atggtcaaat aaaaaaaatg ttcctaaact tggtgatatg aactc      115
302 <210> SEQ ID NO: 19
303 <211> LENGTH: 204
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
309       HUMAN
311 <220> FEATURE:
312 <223> OTHER INFORMATION: n at position 28 is unknown.
314 <400> SEQUENCE: 19
315 gaattcaggg ccgttctggt tctctctntc tccccgccct ccctcaccac cagtggaacc 60
316 ttcatcgagt tccacaaacc tggatttttt atgtacaacc ctgaccgtgg ccgtttgcta 120
317 tattcctttt tctatgaaat aatgtgaatg ataataaaac agctttgact tgaaaaaaaa 180
318 aaaaaaaaag cggccgctga attc                                    204
321 <210> SEQ ID NO: 20
322 <211> LENGTH: 109
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
328       HUMAN
330 <400> SEQUENCE: 20
331 gaattccctc cccctccttg tgccttcttt gtatataggc ttctcacggc gaccaataaa 60
332 cagctcccag tttgtatgca aaaaaaaaaa aaaagcggcc gctgaattc         109
335 <210> SEQ ID NO: 21
336 <211> LENGTH: 191
337 <212> TYPE: DNA
```

W--> 284 (marking in left margin)
W--> 315 (marking in left margin)

VERIFICATION SUMMARY   DATE: 08/06/2001
PATENT APPLICATION: US/09/833,031   TIME: 15:32:38

Input Set : **A:\Gilad2b1.app**
Output Set: **N:\CRF3\08062001\I833031.raw**

```
L:12  M:270 C: Current Application Number differs, Replaced Current Application Number
L:13  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:35  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:35  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:188 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:188 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:190 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:190 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:192 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:192 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:193 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:193 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:194 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:194 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:195 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:195 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:284 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:315 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:315 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:397 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:397 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:457 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:457 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:461 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:461 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:462 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:462 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
```